1/30

cyno3-16 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC TCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC ACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA GAAGACCCCGATGTCAAGTTCAACTGGTACGTAAATGGCGCGGAGGTGCATCATGCCCAGACGAAG CCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAGGAC TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC GACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT (SEQ ID NO. 1) CCGGGTAAA

cyno3-16 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV VEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 'PGK (SEQ ID NO. 2)

2/30

cyno33 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA GCGGCCTGGGCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCCAGCGAGGGAAGGGGGGTGTCTGCTG GAAGCCAGGCTCGGCCTCCTGCCTGGACAAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG GCAGGCCCGTCTGTCTCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA AGCCCACCCAAAGGCCAAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCCCCCACATCCCAGT AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG TCCTCACCGTCACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG CCCTCCCGGCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCG AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCGCCGTGCTGGACTCCGACGGCTCCTAC TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA (SEQ ID NO. 3)

cyno33 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNG QPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK (SEQ ID NO. 4)

3/30

cyno2-4 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCAGGAGCACCTCCGAGAGCACA GCGGCCTGGGCTGGTCAAGGACTACTTCCCCGAACCCGTGACTGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG GAAGCCATGCTCGGCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG GCAGGCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCTCTGCACA CATAGGGGCTGGTGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT AAGCCCACCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC CTCACCGTCACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC CTCCCGGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC TACAGGCCAGCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA CCAGGTCAGCCTGACCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGGAACACCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO. 5)

cyno2-4 amino acid sequence

ASTKGPSVFPLASSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ PENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO. 6)

4/30

cyno2-4cys genomic nucleotide sequence

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCGAGAGCACA GCGGCCCTGGGCTGGTCAAGGACTACTTCCCCGAACCCGTGACTGTGTCGTGGAACTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG GAAGCCATGCTCGGCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCAGCCCAGGGCAGCAGG GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCTCTGCACA CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC CTCACCGTCACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAGGC CTCCCGGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC TACAGGGCAGCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA CCAGGTCAGCCTGACCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGGAACACCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA (SEQ ID NO. 7)

cyno2-4cys amino acid sequence

ASTKGPSVFPLASCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ PENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK (SEQ ID NO. 8)

5/30

cynods1 genomic nucleotide sequence

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA GCGGCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG GAAGCCATGCTCGGCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCTCTGCACA CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCCAGGGACAGGCCC CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAG GTGCATCATGCCCAGACGAAGCCACGGAGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC CTCCCGGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC TACAGGGCAGCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA CCAGGTCAGCCTGACCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA (SEQ ID NO. 9)

cynods1 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ PENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK (SEO ID NO. 10)

6/30

cyno439 cDNA nucleotide sequence

CGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCCTGCTCCAGGAGCACCTC CGAGAGCACAGCGGCCTGGGCTGGCTGATCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTG GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTA CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGT CGTTCATGAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTTCACACGCCCATGTGATGACAC AACTCCCCCATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCGTCTTCCC GAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCACAATGCCCA GACGAAGCCGCGGGAGAGGCAGTTCAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCA CCAGGACTGGCTGAACGCCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCAT CCAGAAAACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTC CATCGTCGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACGCCGCCGTGCT GGACTCCGACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTC CCTGTCTCCGGGTAAATGAGTCGACATGC (SEQ ID NO. 11)

cyno439 amino acid sequence

VSSASTKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTRPCDDTTPPCPPCPAPELLGGPSVFVFP PKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAQTKPRERQFNSTYRVVSVLTVTH QDWLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSD IVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO. 12)

7/30

cyno686 cDNA nucleotide sequence

CGTCTCTAGTCCACCAAGGGCCCATCGGTCTTCCCCCCTGGTGTCCTCCAGGAGCACCTCCGAG AGCACAGCGGCCCTGGGCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAAC TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCC CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTT CATGAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTTCACACGCCCATGTGATGACACAACT CCCCCATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCGTCTTCCCCCCA AAGCCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAG GACTGGCTGAACGCCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAG AAAACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCGGTCCCGG GAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATC GTCGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACGCCGCCCGTGCTGGAC TCCGACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTG (SEQ ID NO. 13) TCTCCGGGTAAATGAGTCGACATGC

cyno686 amino acid sequence

RL*STKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTRPCDDTTPPCPPCPAPELLGGPSVFVFPP KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQ DWLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDI VVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK (SEO ID NO. 14)

8/30

cyno35 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA GCGGCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG GAAGCCAGGCTCGGCCTCCTGCCTGGACAAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG GCAGGCCCCGTCTGTCTCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA! CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG CCCTCCCGGCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGAG TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA (SEQ ID NO. 15)

cyno35 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWESSG QPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK* (SEO ID NO. 16)

9/30

cyno36 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA GCGGCCCTGGGCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG GAAGCCAGGCTCGGCCTCCTGCCTGGACAACTCTGGCTGTGCAGCCCCAGCCCAGGCAGCAGG GCAGGCCCCGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG TCCTCACCGTCACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG CCCTCCCGGCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGGCCCCGGGAGGAGCTGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCG TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA (SEQ ID NO. 17)

cyno36 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNG QPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK* (SEQ ID NO. 18)

10/30

cyno477 cDNA nucleotide sequence

TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCC AGCAACACCAAGGTGGACAAGACAGTTGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGCT GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGATTTCC CGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGAACCCCGATGTCAAGTTCAAC TGGTACGTGGACGCGTGGAGGTGCACAATGCCCAGACAAAGCCGCGGGAGGAGCAGTTCAACAGC ACGTATCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACG TGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCAAGGCAGAAAACTGTCTCCAAAACCAAAGGGCAG CCCCGAGAGCCGCAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAGAACCAGGTCAGC CCGGAGAACACCTACAAGACCACGCCGCCCGTGCTGGACTCCGACGGCTCCTACTTCCTCTACAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGCATGAG GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO. 19).

cyno477 amino acid sequence

STKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEYT CKVSNKALPAPRQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLIKGFYPSDIVVEWASNGQ PENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSLSPGK* (SEO ID NO. 20)

11/30

cyno32 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA GCGGCCCTGGGCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG GAAGCCAGGCTCGGCCTCCTGCCTGGACAACTCTGGCTGTGCAGCCCCAGCCCAGGCAGCAGG GCAGGCCCGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA CACAGGGGCAGGTGCTGGGCTCAGGCCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA AACTCCCAATCTTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA GGCCCTGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGGACCGT CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAACTTCAACTGGTACGTGGACGGCGTGG AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG TCCTCACCGTCACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG GCCTCCCGGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGC CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC CCTACAGGGCAGCCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAG ${\tt TTCCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGGAACACCTTCTCATGCTCC}$ GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA (SEQ ID NO. 21)

cyno32 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY TCKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNG QPENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK* (SEQ ID NO. 22)

12/30

cyno3-18 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA $\tt GCGGCCCTGGGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC$ TCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAACATGTGGTGGTGGCAGCAAACCTCCCACG TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTTCCCCCCAAAACCC GACCCCGATGTCAAGTTCAACTGGTACGTAAATGGCGCGGAGGTGCATCATGCCCAGACGAAGCCA CGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAGGACTGG CTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAGCCCTCCCGGCCCCCATCCAGAAAACC ATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCGGTCCCGGGAGGAG CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTG GGCTCCTACTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEO ID NO. 23)

cyno3-18 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEITCGGGSKPPTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDW LNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVV EWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK (SEQ ID NO. 24)

13/30

cyno1-3 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC ACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAG GAAGACCCCGAGGTCCAGTTCAACTGGTACGTAAACGGCGCGGAGGTGCATCATGCCCAGACGAAG CCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGAC TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCGTCCCGGGAG GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC GACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT (SEQ ID NO. 25) CCGGGTAAA

cyno1-3 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV VEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLŞLS PGK (SEQ ID NO. 26)

14/30

cyno1-4 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC ACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAG GAAGACCCCGAGGTCCAGTTCAACTGGTACGTAAACGGCGCGGAGGTGCATCATGCCCAGACGAAG CCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGAC TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCGTCCCGGGAG GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC GACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT (SEQ ID NO. 27) CCGGGTAAA

cyno1-4 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV VEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK (SEQ ID NO. 28)

15/30

cynoKappa cDNA nucleotide sequence

CGCGCTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGAGGATCAGGTGAAATCTGGAACT
GTCTCTGTTGTGTGCCTGCATAAACTTCTATCCCAGAGAGGCCAGCGTAAAGTGGAAGGTGGAT
GGTGTCCTCAAAACGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAACACCTAC
AGCCTGAGCAGCACCCTGACGCTGAGCAGCACAGACTACCAGAGTCACAATGTCTATGCCTGCGAA
GTCACCCATCAGGGCCTGAGCTCGCCCGTCACCAAGAGCTTCAACAGAGGAGAGTGTTAGB
(SEQ ID NO. 29)

cynoKappa amino acid sequence

RAVAAPSVFIFPPSEDQVKSGTVSVVCLLNNFYPREASVKWKVDGVLKTGNSQESVTEQDSKDNTY SLSSTLTLSSTDYQSHNVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO. 30)

A. Nucleotide sequence alignments

			•
_cyno33 _cyno35 _cyno477 _cyno32	_cyno33 _cyno35 _cyno477 _cyno32	_cyno33 _cyno35 _cyno477 _cyno477	_cyno33 _cyno35 _cyno36 _cyno477
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTCCAGGAGCACCTCCCAGAGCACAGGGGCCCTGGGCTGCTGGTCAAGGACTACTTCC GCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACAGGGCCCTGGGCTGCTGAAGGACTACTTCC GCCTCCACCAAGGGCCCATCGGTCTTCCCCTTGGTGTTCTGTTCCAGGAGCACCTCCCAGAGCACAGGGCCTTGGGCTGCTGGTCAAGGACTACTTCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCGTCCTGCTCCAGGAGCACAGAGCACAGGGCCTGGGCTGGTCAAGGACTACTTCC GCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCGTCCTGCTCCAGGAGCACAGAGCACAGGGCCCTGGGCTGGTCAAGGACTACTTCC GCCTCCACCAAGGGCCCATCGGTCTTTCCCCTGGCGTCCTGGTCCTCCAGGAGCACAGGGCCCTGGGCCTGGTCAAAGGACTACTTCC GCCTCCACCAAGGGCCCATCGGTCTTTCCCCTGGCTCGTCCTGGTCCTTCC GCCTCCACCAAGGGCCCCATCGGTCTTTCCCCTGGGGGACACAGGGGCCCTGGGCCTGGTCAAAAAAAA	110 120 130 140 150 160 170 180 190 200 CCGAACCCGTGACCGTGACCTGACCGTGACCAGCGGCGTGCACCCTTCCGAGGCTGTCCTCAGGGCTCTCAGGGCTCTCAGGCAG CCGAACCCGTGACCGTGTCGTGGAACTCAGGCGCCCTGACCAGGGCTGCACACCTTCCAGGGCTGTTCCTTCAGGGCTCTTACTCCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGGCTCTCAGGCAGCGCAGCCGTGCAGGCGCTCTCAGGGGCTCTCAGGGGCTCTCAGGGGCTCTCAGGGAGCTCTCAGGGGCTCTCAGGCAGG	CGTGGTGACCGTCCAGCAGCTTGGGCACTCAGACCTCAGCACGTCATCATGAGCCCAGCAACGCGAAGTGGCCAAGGTGGCTC CGTGGTGACCGTGCCTCCAGCAGCTTGGGCACTAGACCTCAGCAACGTCATCATGAGCCCAGCAACGTGGACAAGACAGTTGGGCTC CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCTCAGAACGTCGTTCATGAGCCCAGCAACAGTGGACAAGATGGACTC CGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCAGAACGTCTGCAACGTTCATGAGCCCÁGCAAGGTGGACAAGATGGACTTGGGCTC CGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCTAGAGCTTGCAACGTTCATGAGCCCÁGCAAGGTGGACAAGATGGACTTGGGCTC CGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTTGCAACGTTCATGAGCCCAGCAACGTGGACAAGACAAGACAAGACTTGGGCTC CGTGGTGACCGTGCCTCCAGCAGCTTGGGCCAGACCTTGCAACGTTCATGAGCCCAGCAACGTGGAAGATGGGCTC CGTGGTGACCGTCCAGCAGCTTGGGCACCCAGACCTCACAACAACAACAACAACAAGAGTGGACAAGAAGAAGAAGACTTGGGCTC CGTGGTGACCGTGCAACACAACA	310 320 330 400 CCATGTCGTCGTCGTGAGCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACCGTGCCCAGCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACGTGCCCAGCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAGCACAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACGTGCCCAGCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACGTGCCCAGGTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTTCCCCCCAAAACCCCAAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACCTGAACTCCTGGGGGGGACCGTCAGTCTTTCCTCCTTTCCCCCCAAAACCCCAAGGACACCCTCATGATTTCCC CCATGTCGTTCCACGTGCCCACCTTGAACTCCTTGGGGGGGACCGTCAGTCTTTCCCCCCAAAACCCCAAGGACACCCTCATGATTTCCC CCATGTCACACTACCACGTGCCCACCTTGAACTCCTTGGGGGGGACCCTCTTCCTTC
_cyno33 _cyno35 _cyno36 _cyno477 _cyno32	_cyno33 _cyno35 _cyno477 _cyno32	_cyno33 _cyno35 _cyno477 _cyno477	_cyno33 _cyno35 _cyno36 _cyno477

FIG. 16A

	410	420	430	440	450	460	470	480	490	200	
супозз	GGACCCCTGAGGTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGAAGGAA	rcacerecere	GEGGEAGACC	srcagccago.	AAGAACCCGAT	STCAAGTTCA	ACTGGTACGT	3GAÇGGCGTG	AGGTGCACAA	•	_cyno33
_cyno35	GGACCCCTGAGGTCACGTGGTGGTAGACGTGAGCCAGGAAGAACCCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCCA	rcacerecere	SGTGGTAGACC	FFGAGCCAGG2	AAGAACCCGAT	FICAAGITICA	ACTGGTACGT	SGACGGCGTGG	AGGTGCACAA	TGCCCA	_cyno35
_cyno36	GGACCCCTGAGGTCACGTGGTGGTAGACGTGAGGAAGAACAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAATGCCCA	rcacerecere	SGTGGTAGACC	TGAGCCAGG	AGAACCCGAT	STCAAGTTCA	ACTIGGTACGT	зедсеесетес	AGGTGCACAA		_cyno36
_cyno477	GGACCCCTGAGGTCACGTGGTGGTGGTGACGTGAGCCAGGAAGAACCCGATGTTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCCA	rcacetecere	GTGGTGGACC	TGAGCCAGG	AAGAACCCGAT	STCAAGTTCA	ACTGGTACGT	SGACGGCGTGG	AGGTGCACAA		_cyno477
_cyno32	GGACCCTGAGGIYCACGITGCGITGGTGGTGGTGAAGCCAGGAAGCAAACCCGAATGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCCA	rcacerecere	SCTCGTAGACC	TGAGCCAGG	AAGAACCCGAT	STCAAGITICA	ACTIGGTACGT	зедсвесетве	AGGTGCACAA	TGCCCA	_cyno32
	医哈拉格格拉格格拉格格拉格格拉格格拉格格拉格格格格 医艾尔氏试验检尿液溶液 医阿拉拉氏试验检尿病检验检尿病检验检尿病检验检验检验检验检验检验检验检验检验检验检验检验检验	****	***	***	***	* * * * * * * * * * * * * * * * * * * *	***	****	****	* * * *	
	510	520	530	540	550	260	570	580	590	009	
_cyno33	GACGAAGCCACGGGAGCAGTTCAACAGCATGCATGCTGGTCAGCGTCCTCACCGTCATCACAGACAG	GRAGGAGCAGT	FTCAACAGCAC	GTACCGCGTK	SGTCAGCGTCC	rcaccercac	ACACCAGGAC	rGGCTGAACGC	CAAGGAGTAC	ACGTGC	_cyno33
_cyno35	GACGAAGCCACGGGAGGAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCGTCACACACA	SGAGGAGCAGT	FTCAACAGCAC	GTACCGCGT	3GTCAGCGTCC	rcaccercac	ACACCAGGAC	rGGCTGAACGC	SCAAGGAGTAC	ACGTGC	_cyno35
_cyno36	GACGAAGCCACGGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTCCTCACACACA	3GAGGAGCAG	TTCAACAGCAC	GTACCGCGT	SGTCAGCGTCC	rcaccercac	ACACCAGGAC	recerenace	CAAGGAGTAC	ACGTGC	_cyno36
_cyno477	GACAAAGCCGCGGGGAAGCAGCAGTACAACAGCACGTATCGCGTGGTCAGCGTCCTCACCGTCACACACA	GEAGGAGCAG	FTCAACAGCAC	GTATCGCGTC	GICAGCGICC	PCACCGTCAC	ACACCAGGAC	rescteaacs	SCAAGGAGTAC	ACGTGC	_cyno477
супо32	GACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCACCACCACCACCACACACA	3 ĠAGGAGCAG1	TTCAACAGCAC	GTACCGCGTC	SGTCAGCGTCC	PCACCGTCAC	ACACCAGGAC	reccteaace	SCAAGGAGTAC	ACGTGC	_cyno32
	南部的 化安托拉克 化水油化物化水油水油化物水油水油水油水油水油水油水油水油水油水油水油水油水油水油	****	****	* * * * * * * * * * * * * * * * * * * *	****	****	***	***	****	* * * *	
	610	620	630	640	650	099	670	680	069	700	
_cyno33	AAGGTCTCCAACAAAGCCCTCCCGGGCCCCAAAAGCAGAAAACTGTCTCCAAAAGGGGCAGGCCGGAGGGCCACAGGGGTGTACACCCTGCCCCGGCCCC	AAAGCCCTCC	CGGCCCCAAAG	SCAGAAAACT	STCTCCAAAAC	CAAAGGGCAG	CCCCGAGAGC	ACAGGEGERA	ACCCTGCCC		_cyno33
_cyno35	AAGGTCTCCAACAAAAGCCCTCCCGGGCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAAGGGCAGCCCCGGAGAGGCCACAGGTGTACACCCTGCCCCGGCCCCC	AAAGCCCTCC	CGGCCCCAAAG	SCAGAAAACTK	FTCTCCAAAAC	CAAAGGGCAG	CCCCGAGAGC	PACAGGTGTAC	ACCCTGCCCC	ವಾದಾದ	_cyno35
_cyno36	AAGGTCTCCAACAAAAAGCCCTCCCGGCCCCAAAAGCAGAAAACTGTCTCCAAAACCAAAAGGGCÄGCCCCGAAGAGCCACAGGTGTACACCCTGCCCCGCCCC	AAAGCCCTCC	CGGCCCCAAAC	SCAGAAAACTO	Prcrccaaaac	CAAAGGGCAG	CCCCGAGAGC	CACAGGTGTAC	ACCCTGCCCC	. כפככככ	_cyno36
_cyno477	AAGGTCTCCAACAAAAGCCCTCCCGGCCCCAAGGCAGAAAACTGTCTCCAAAACCAAAAGGGCAGCCCCGGAGAGCCGCAGGTGTACACCCTGCCCCGCCCC	AAAGCCCTCC	CGCCCCAAGC	SCAGAAAACTO	STCTCCAAAAC	CAAAGGGCAG	CCCCGAGAGC	Э ВСА БВТВТА С	ACCCTGCCCC	သသသသ	_cyno477
_cyno32	AAGGTCTCCAACAAAAGGCCTCCCGGCCCCCCATCGAGAAACCATCTCCAAAGGCAAAGGCAGGC	AAAGGCCTCC	ceccicican	GAGAAAACC	ATCTCCAAAGO	CAAAGGGCAG	CCCCGAGAGC	сесместетм	ATCCTGCCCC	သသသသ	_cyno32
	我 化苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基苯基	***	* * * *	* * * * *	法非年代法律 医法法氏性检查法 化异丙烯二甲异丙烯二甲异丙烯二甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲	***	****	***	***	* * * *	
•	710	720	730	740	750	160	770	780	190	800	
_cyno33	GOGAGAGCAGCTGACCAAGATCAAGCCTGATCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGAGAGGAGAGAGA	CCAAGAACCAC	GETCAGCCTG	ACCTGCCTGG	rcaaaggcttc	TACCCCAGCG	асатсетсет	3GAGTGGGCG1	AGCAACGGGCA	GCCGGA	_cyno33
_cyno35	GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG	CCAAGAACCAG	GGTCAGCCTG2	ACCTGCCTGG	ICAAAGGCTTC	raccccagcg	ACATCGTCGT	3GAGTGGGAG 2	AGCAGCGGGCA	GCCGGA	_cyno35
_cyno36	GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTCCAAAAGGCTTCTACCCCAGCGACATCGTCGAGGAGTGGGCGAACAACGGGCAACCGGA	CCAAGAACCA	GETCAGCCTG	ACCTGCCTGG	rcaaaggct rc	PACCCCAGCG	ACATCGTCGT	3GAGTGGGCG2	GCAACGGGCA	GCCGGA	_cyno36
_cyno477	GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTGATCAAAGGCTTCTACCCCAGCGACATCGTGGAGTGGGCGAGAACGGGCAGCAGCAGCAGCAGCAGCAGCAG	CCAAGAACCA	GGTCAGCCTG?	асстесства:	<i>PCAAAGGCTTC</i>	TACCCCAGCG	ACATCGTCGT	3GAGTGGGCG2	AGCAACGGGCA	GCCGGA	_cyno477
_cyno32	AGGAGGAGCTGACCAAGAACCAGGTCAGCCTGCTTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGAACGGGCAGCCGGA	CCAAGAACCA	GETCAGCCTG	ACCTGCCTGG	<i>PCACAGGCTTC</i>	TACCCCAGCG	ACATCGCCGT	3GAGTGGGAG	AGCAACGGGCA	GCCGGA	_cyno32
	法非法律法法法法法法 电电影电子 电光光电影电影光光电话 医非水类性性性性性性性性性性性性性的 有效 医苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基苯甲基	********	*********	*******	*** ***	********	*** *****	*****	***** ***	*****	

FIG. 16B

_cyno33 _cyno35 _cyno36 _cyno477 _cyno32	810 820 890 900 GAACACCTACAAGACCACCCCGCCGTGGTGGACGCTCGTACGACGCTACACGTGGACAAGAGCAGAGAGCTGGAGGGGAACcynô33 GAACACCTACAAGACCACCCCGCCCGTGGTGGACGGCTCCTACTTCCTCTACAGCAAGCTGGACAAGAGCAGGAGGAACcynô35 GAACACCTACAAGACCACCCGCCCGTGGTGGACGGCTCCTACTTCCTCTACAGCAAGAGCTGGACAAGAGCAGGGGAACcyno35 GAACACCTACAAGACCAGCCGCCGTGCTGGACGGCTCCTACTTCCTCTACAGCAAGAGCTCGGACAGAGCAGGGGGAACcyno36 GAACACCTACAAGAACCACGCCGCCGTGCTGGACGGCTCCTACTTCCTCTACAGCACGAGGCTGGACAGAGCAGGGGGAACcyno36 GAACACCTACAAGAACCACGCCGGCCGGTGCTGGACGGCTCCTACTTCCTCTACAAGCTCACGTGGACAGGGGGGAACcyno37 GAACACCTACAAGAACAACAACAACAACAACAACAAGAGCTGGCAGCAGGGGAACcyno37 ***********************************	820 CCACCCCGO CCACCCCGO CCACCCCGO CCACCCCGO	830 CCGTGCTGGA CCGTGCTGGA CCGTGCTGGA CCGTGCTGGA	840 zrccgaceec zrccgaceec zrccgaceec zrccgaceec	850 ICCTACTTCC ICCTACTTCC ICCTACTTCC ICCTACTTCC	860 ICTACAGCAAC ICTACAGCAAC ICTACAGCAAC	870 GCTCACCGTGG GCTCACCGTGG GCTCACCGTGG GCTCACCGTGG	880 JACAAGAGG JACAAGAGG JACAAGAGG JACAAGAGG JACAAGAGG	890 aggregeracea	900 GGGGAAC GGGGAAC GGGGAAC GGGGAAC GGGGAAC	_cynó33 _cyno35 _cyno36 _cyno477 _cyno32
	910	920	930	940	950	096	970	980			
_cyno33	ACCTICTOATGCTCCGTGATGCATGAGGCTCTGCACACACACACCAGAAGAGGCCTCTCCGGGTGTCTCCGGGTAAA	CGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACCCAGAA	SAGCCTCTCC	Grercrees		_cyno33		
Cyno35	ACCITICICATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGGTGTCTCCGGGTAAATGA	CGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACCCAGAA	BAGCCTCTCC	Grercreese		_cyno35		
cyno36	ACCTICTOATGCTCCGTGATGCATGAGGCTCTGCACAAACCACAAAGAAGAAGAACCTCTCCGTGTCTCCGGGTAAATGACyno36	CGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACCCAGAA	SAGCCTCTCC	GTGTCTCCGG	TAAATGA	_cyno36		
_cyno477	ACCITICICATGCTCCGTGATGCGTGTGAGGCTCTGCACACCACTACACCAGAAGAGCCTCTCTCT	CGTGATGCA	TGAGGCTCTG	TACAACCACT	ACACCCAGAA	SAGCCTCTCC	CTGTCTCCGG	STAAATGA	_cyno477		
cyno32	ACCITICIOAIGCICCGIGAIGCAIGAGGCICTGCACACACACTACACCCCAGAAGAGCCTICCGGIGATATAATGACYNO32	CGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACCCAGAA	SAGCCTCTCC	GTGTCTCCGG	STAAATGA	_cyno32		
·	法被诉讼法律法法法法法 人名英格兰人姓氏 医克里氏病 医克里氏病 医克里氏病 医克里氏病 医克里氏病 医克里氏病 计多数记录器 医克里氏病 计多数记录器 医多种性原因 计多数记录器 计记录器 计多数记录器 计多证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证证	*****	****	******	*****	******	********	****			

B. Nucleotide	B. Nucleotide sequence alignm										
cyno2-4 _ cyno2-4cys _cynods1 _cyno686 _cyno6439	GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCAGGAGCACCTCCGAGAGCACCAGGGCGCCCTGGGCTGGTCAAGGACTACTTCCcyno4_2 GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCTAGGAGCACCACCAGGAGCACCACTGGCTCGGTCAAGGACTACTTCCcyno4_2 GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCTCCTGGTCCAGGAGCACCACGAGAGCACACGGGCTGCTGGTCAAGGACTACTTCCcyno2_4GsTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCTGGTCAAGGACTACTTCCcyno439 GCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCCTGGTGCTCCAGGAGCACCTCGGTCAAGGACTACTTCCcyno439 ***********************************	SCCCATCGG SCCCATCGG SCCCATCGG SCCCATCGGI	ICTRCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCCTK ICTRCCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCCTK ICTRCCCTK ICTRCCCCTK ICTRCCCTK ICTRCCTK ICTRCCCTK ICTRCCTK ICTRCCCTK ICTRCCTCT ICTRCCTT	SECETCETCET SECETCETCET SECETCETCET SETETCETCETCET SETETCETCETCET SETETCETCETCETCETCETCETCETCETCETCETCETCET	CCAGGAGCACC CCAGGAGCACC CCAGGAGCACC CCAGGAGCACC CCAGGAGCACC	TCCGAGAGC TCCGAGAGC TCCGAGAGC TCCGAGAGC TCCGAGAGC	ACAGCGGCCC ACAGCGGCCC ACAGCGGCCC ACAGCGGCCC ACAGCGGCCCC ACAGCGGCCCC	TGGGCTGCCTN TGGGCTGCCTN TGGGCTGCCTN TGGGCTGCCTN	CATCGGTCTTCCCCCTGGCGTCCTCCAGGAGCACCTCCGAGAGCACAGGGGCCCTGGGCTGCCTGGTCAGGACTACTTCC CCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCGAGAGCACAGGGGCCCTGGGCTGCTTGGTCAAGGACTACTTCC CCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTTGGGCTGCTGGTCAAGGACTACTTCC CCATCGGTCTTCCCCCTGGTGTCTCCTGCTCCAGGAGCACCTCCGAGAGCACAGGGGCCTGGGCTGGTCAAGGACTACTTCC CCATCGGTCTTCCCCCTGGTGTCTCCAGGAGCACTCCGAGAGCACACAGGGCCTGGGCTGGTCAAGGACTACTTCC CCATCGGTCTTCCCCCTGGTGTCCTCCAGGAGCACTCCGAGAGCACACAGGGCCTGGGCTGGTCAAGGACTACTTCC CCATCGGTCTTCCCCCTGGTGCTCCAGGAGCACTCCGAGAGCACACACA	Tricc - cylinger - cyl	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno686
_cyno2-4 _ cyno2-4cys _ cyno686 _cyno686 _cyno6439	CCGAACCCGTGACTGTGTGGTGGCGCCCTGACCAGGGGGTGCACACCTTCCGGCTGTCCTACAGGGCTCTACAGGGCTCTACAGGACCCTCAGCAGCACCCTCAGCAGCGCTGTCCTCAGGGGCTCTACTCCCTCAGGCAGCACCCTCAGCAGCCCTCAGCAGCCCTCAGGCGCTCTACAGGGCTCTACAGGGCTCTACAGCAGCAGCAGCAGCAGCAGCTGTCCTAGGGGCTCTACAGGGGCTCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 rerercered rerercered cerercered cerercered	130 gaactcaggcc gaactcaggcc gaactcaggcc gaactcaggcc	140 sccraaccae sccraaccae sccridaccae sccridaccae	150 ceecerecaca ceecerecaca ceecerecaca ceecerecaca	160 ACCTTCCCGG ACCTTCCCGGG ACCTTCCCGGG	170 CTGTCCTACA CTGTCCTACA CTGTCCTACA CTGTCCTACA	180 erccrcaeee erccrcaeee erccrcaeee erccrcaeee	190 CTCTACTCCTCA CTCTACTCCTCA CTCTACTCCCTCA CTCTACTCCCTCA	200 GCAGC; GCAGC; GCAGC; GCAGC; GCAGC;	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno439

cyno2-4 cyno2-4cys cyno686 cyno686	210 220 230 290 300 CGTGGTGACCGTGCCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGCAACGTGGACGAAGAGAGAG	210 220 230 290 300 CGTGGTGACCGTGCCCCCCAGACCTACGTCTGCAACGTTCATGAGCCCAGCAACACCCAAGGTGGACAAGAGAGTTGAGTTC CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCTACGTCTTGCATCGTTCATGAGCCCAGCAACACCCAAGGTGGACAAGAGTTGAGTTC CGTGGTGACCGTGCCCTCCAGCAGCTTTGGGCACCTAGATCGTCTTGATCATCATGAGCCCAGCAACACCCAAGGTGAAGAGATTTGATTTC CGTGGTGACCGTGCCCTCCAGCACCTTTGGGCACCTAGATCTCTTGATCATTCAT	20 240 250 260 270 280 290 300 CAGCAGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGCAACAAGGTGGACAAGGAGTTGAGTTC CAGCAGCTTGGGCACCCAGACGTCGTTCATGAGCCCAGCAACACCCAAGGTGGACAAAGAGTTGAGTTC CAGCAGCTTGGGCACCCAGACCTACGTCTGCTTCATGAGCCCAGCAACACACAGGTGAAAAAAAA	240 CAGACCTACG CAGACCTACG CAGACCTACG CAGACCTACG CAGACCTACG	250 TCTGCAACGI TCTGCAACGI TCTGCAACGI TCTGCAACGI	260 CGTTCATGAG CGTTCATGAG CGTTCATGAG CGTTCATGAG	270 CCCAGCAAC? CCCAGCAAC? CCCAGCAAC? CCCAGCAAC?	280 CCAAGGTGG CCAAGGTGG CCAAGGTGG	290 ACAAGAGAGTT ACAAGAGAGTT ACAAGAGAGTT ACAAGAGAGTT ACAAGAGAGTT ACAAGAGAGTT ACAAGAGAGTT	300 IGAGTTC IGAGTTC IGAGTTC IGAGTTC	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686
cyno2-4 _ cyno2-4cys _ cynods1 _cyno686 _cyno439	310 ACAC ACAC ACAC ACACGCCCATGT ACACGCCCATGT ACACGCCCATGT	320 320 30 30 30 30 30 30 30 30 30 30 30 30 30	1310 340 350 350 350 350 350 350 350 350 350 35	340 CACCATGCCC CACCATGCCC CACCATGCCC CACCGTGCCC	AGCACCTGAR AGCACCTGAR AGCACCTGAR AGCACCTGAR AGCACCTGAR	CTCCTGGGGG CTCCTGGGGG CTCCTGGGGG CTCCTGGGGGG	570 SGACCGTCAGT SGACCGTCAGT SGACCGTCAGT SGACCGTCAGT	CTTCCTCTT CTTCCTCTT CTTCGTCTT CTTCGTCTT	SSU		_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno639
cyno2-4 cyno2-4cys cynods1 cyno686 	410 420 430 440 450 500 ACACCCTCATGATCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTGGAGGAGGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCTGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGAAGAGCCCGAAGGTCCAGTTCAACTGGTACGTGGACGGCGT ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCTGGTGGTGGTGGACGTAGGAAGAGCCCGAAGGTCCAGTTCAACTGGTACGTGGACGCGT ACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGTGGACGTAGGAAGACCCCGAAGATCCAGTTCAACTGGTACGTGGACGCGC ACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGTGGTGGTGGTAGGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACACTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACACTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACACACACACACACACACACACACACACACACACACACAC	ALO 420 430 440 450 460 500 500 ACACCCTCATGATCCCGGACCCCTGAGGTCATGCGTGGTGGTGGTGGTGGAGGCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTcyno4_2 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGGTGGAGGCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTcyno4_2 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGAGACGCCGAGGTCCAGTTCAACTGGTACGTAC	20 430 440 450 460 500 GGACCCCTGAGGTCATGAGGGGGGGGGGGGGGGCCAGGTCCAGTTCAACTGGTAGGACGCCGGGGGCCCTGAGGTCCAGTTCAACTGGTAGGACGCCGGGGCCCCTGAGGTCCAGTTCAACTGGTAGGTGGACGCCGGGACCCCTGAGGTCCAGTTCAACTGGTAGGTGGTGGACGCCGGGACCCCGGAGGTCCAGTTCAACTGGTAGGTA	440 ATGCGTGGTG ATGCGTGGTG ATGCGTGGTG ATGCGTGGTG GTGCGTGGTG GTGCGTGGTG ATGCGTGGTG ATGCGTG ATG	450 icrogaccrost icrogaccrost icrogaccrost icrogaccrost icrogaccrost	460 GCCAGGAAG GCCAGGAAG GCCAGGAAG GCCAGGAAG	470 ACCCCGAGGTC ACCCCCGAGGTC ACCCCGAGGTC ACCCCGAGGTC ACCCCGAGGTC ACCCCCGAGGTC ACCCCCCGAGGTC ACCCCCCGAGGTC ACCCCCCGAGGTC ACCCCCCGAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCAGGTC ACCCCCCAGGTC ACCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCCAGGTC ACCCCCC	480 CAGTTCAAC CAGTTCAAC CAGTTCAAC	490 TGGTACGTGG TGGTACGTGG TGGTACGTGGTACGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTGGTACGTAC	500 ACGGCGT ACGGCGT ACGGCGT ACGGCGC	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno686
	510 GGAGGTGCATC GGAGGTGCATC GGAGGTGCATC GGAGGTGCATC GGAGGTGCATC	GGAGGTGCATCATGCCCAGAGGCAAGCCAGGAAGAGGCAGTTCAACAGCACGTACCGGCTGGTCAGGCGTCACGTCACACACA	530 AAGCCACGGGAC AAGCCACGGGAC AAGCCACGGGAC AAGCCACGGGAC AAGCCACGGGAC	540 saggcagtica saggcagtica saggcagtica sacgcagtica sacgcagtica sacgcagtica sacgcagtica	550 ACAGCACGTZ ACAGCACGTZ ACAGCACGTZ ACAGCACGTZ ACAGCACGTZ ACAGCACATZ ACAGCACATZ	560 ACCGCGTGGTA ACCGCGTGGTA ACCGTGTGGTA ATCGTGTGGTA	570 zaccercerc zaccercerc zaccercerc zaccercerc zaccercerc zaccercerc	580 ACCGTCACAC ACCGTCACAC ACCGTCACAC ACCGTCACAC ACCGTCACAC	590 ACCAGGACTG ACCAGGACTG ACCAGGACTG ACCAGGACTG ACCAGGACTG ACCAGGACTG	600 SCTGAAC SCTGAAC SCTGAAC SCTGAAC	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno639

FIG. 16D

_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno686	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno686	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686 _cyno639	_cyno4_2 _cyno4_2cys _cyno2_4ds _cyno686
700 AGGTGT AGGTGT AGGTGT AGGTGT	800 GTGGGA GTGGGA GTGGGA GTGGGA	900 AAGAGC AAGAGC AAGAGC AAGAGC	AATGA AA AATGA AATGA
690 CCGAGAGCCGCZ CCGAGAGCCGCZ CCGAGAGCCGCZ CCGAGAGCCCCZCZ CCGAGAGCCCCZCZCZCZCZCZCZCZCZCZCZCZCZCZCZ	790 ATCGCCGTGGAA ATCGCCGTGGAA ATCGCCGTGGAA ATCGTCGTGGAA ATCGTCGTGGAA	890 TCATCGTGGAC TCATCGTGGAC TCATCGTGGAC TCACCGTGGAC TCACCGTGGAC	990 GTCTCCGGGTA GTCTCCGGGTA GTCTCCGGGTA
680 AGGGCAGCC AGGGCAGCCC AGGGCAGCCC AGGGCAGCCC	780 cccagcacc cccagcacc cccagcacc cccagcacc cccagcaccacc	880 ACAGCAAGC ACAGCAAGC ACAGCAAGC ACAGCAAGC ACAGCAAGC	980 CCTCTCCGT CCTCTCCGT CCTCTCCGT CCTCTCCCT
670 CCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGC	0 730 740 750 800 800 GGASGASGASASASASASASASASASASASASASASASA	870 CTACTTCCTCT CTACTTCCTCT CTACTTCCTCT CTACTTCCTCT CTACTTCCTCT	CCTTCTCATGCTCCGTGATGCATCACCACAACCACTACACCCCAGAAGAGCCTCTCCGTGTCTCCGGGTPAAA CCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACCCCAGAAGAGCCTCTCCGTGTCTCCGGGTPAAA CCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTPAAA TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAAA TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAA
660 AAAACCATC AAAACCATC AAAACCATC AAAACCATC	760 accredrca accredrca accredrca accredrca accredrca	860 CGACGGCTC CGACGGCTC CGACGGCTC CGACGGCTC	960 AACCACTAC PACCACTAC PACCACTAC PACCACTAC PACCACTAC PACCACTAC PACCACTAC
650 CCCCATCGAGI CCCCCATCGAGI CCCCCATCGAGI CCCCCATCGAGI CCCCATCGAGI CCCCATCCAGI	750 CAGCCTGACCT	850 GTGCTGGACTC GTGCTGGACTC GTGCTGGACTC GTGCTGGACTC	950 pagecrerecae pagecrerecae pagecrerecae pagecrerecae pagecrerecae
640 GCCTCCGG GCCTCCGG GCCTCCGG CCCTCCGG	740 GAACCAGGT GAACCAGGT GAACCAGGT GAACCAGGT	840 paccaecca paccaeccaeccaeccaeccaeccaeccaeccaeccaecc	940 FIGALGCÁTC FIGALGCATC FIGALGCATC FIGALGCATC
630 TCCAACAAGA TCCAACAAG TCCAACAAG TCCAACAAG	730 AGCTGACCAA AGCTGACCAA AGCTGACCAA AGCTGACCAA	830 CCTACAAGACC CCTACAAGACC CCTACAAGACC CCTACAAGACC CCTACAAGACC	930 TCATGCTCCC TCATGCTCCC TCATGCTCCC
620 grączadgerci grączagerci grączagerci grączagerci	720 ccccagagag ccccagagag ccccagagagagarccagagagagagagagagagagagag	820 cccacaacac cccacaacac cccacaacac cccacaaca	920 SGAACACCTTC SGAACACCTTC SGAACGTCTTC SGAACGTCTTC
610 620 630 700 GGCAAGGAGTACCAAGGAGACAAAGGCCTCCGGCCCCATCGAGAAACCATCTCCAAAGGGCAGCCCCGAGAGGCCCCGAGGTGTcyno4_2 GGCAAGGAGTACACGTGCAAGATCTCCAACAAAGGCCTCCCGGCCCCCATCGAGAAACCATCTCCAAAGGGCAAGGCCCCGAGAGGCCGCAGGTGTcyno4_2 GGCAAGGAGTACACGTGCAAGATCTCCAACAAAGGCCTCCCGGCCCCCATCGAGAAACCATCTCCAAAGGCCAAAGGGCAGGCCCCGAGAGGCGCAGGTGTcyno2_4 GGCAAGGAGTACACGTGCAAGAAGACCTCCCGGCCCCCATCCAGAAAACCATCTCCAAAGACCAAAGGCCCGAGAGCCTCAGGTGTcyno686 GGCAAGGAGTACACGTGCAAAGAGCCTCCCGGCCCCCATCCAGAAAACCATCTCCAAAGAGACAAAGGCCCCGAAGAGCTCAAGGTGTcyno686 GGCAAGGAGGAACACGTGCAAAGAAACACAAAAAAAAACAAAAAAAA	ACATCCTGCCCCCGCCCAGGAGGAGCTCAAGAACCAGGTCAGCTGACCTGCTCACCAGGCTACCCCCAGCGACATCGCCGTGGAGTGGGAAACCTGCCTG	810 820 830 840 850 860 870 870 880 800 900 900 gagccagcagcagcagcagcagcagcagcagagaagcagagaaga	AGGTGGCAGCAGGGGAACACCTTCTCATGCTCGTGATGCATGAGGCTCTGCACACACCACACACA
cyno2-4 cyno2-4cys cyno6s1 cyno686 cyno439	_ cyno2-4 _ cyno2-4cys _ cyno681 _cyno686 _cyno439	_ cyno2-4 _ cyno2-4cys _ cynods1 _cyno686 _cyno439	cyno2-4 _cyno2-4cys cyno686 _cyno686

FIG. 16E

C. Nucleotide sequence alignments

10 20 30 GCCTCCACCAAGGGCCCATGGGTCTTCCCCCT GCCTCCACCAAGGGCCCATGGGTCTTCCCCCT GCCTCCACCAAGGGCCCATGGGTCTTCCCCCT GCCTCCACCAAGGGCCCATGGTCTTCCCCCT **************************
20 GGGCCCATCGGTCTT GGGCCCATCGGTCTT GGGCCCATCGGTCTT ACCGTGTCGTGGAAC ACCGTGTCGTGGCAAC ACCGTGTGTCGTGGCT ACCGTGTCGTGGCAAC ACCGTGTGGCAAACC ACGGTGGCAAACC ACGGTGGCAACC ACGGTGGCAAACC ACGGTGGCAAACC ACGGTGGCAACC ACGGTGGCAACC ACGTGTGCAACC ACGGTGGCAACC ACGGTGGCAACC ACGGTGTGCACACACC ACGGTGCACACACC ACGGTGTGCACACACC ACGGTGTGCACACACC ACGGTGTGCACC ACGTGTGCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACACC ACGGTGTCACC ACGGTGTCACC ACGGTGTCACACC ACGGTGTCACC ACGGTG
10 GCTCCACCAAGGGC GCCTCCACCAAGGGC GCCTCCACCAAGGGC GCCTCCACCAAGGGC GCTCCACCAAGGGC GCTCCACCAAGGCC CTGAACCCGTGACC CTGAACCCGTGACC CTGAACCCGTGACC CGTGGTGACCGTGCC AAAACATGTGGTGGTGGT AAAACATGTGGTGGTGGT AAAACATGTGGTGGTGGT AAAACATGTGGTGGTGGT

FIG. 16F

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_cyno3_18 _cyno3_16 _cyno1_3	_cyno1_4	_cyno3_18	_cyno3_16	_cyno1_3 _cyno1_4
500 PAATGG PAATGG	AAACGG	600 TGGCTG	TGGCTG	TGGCTG
490 SAACTGGTACGT SAACTGGTACGT	:***********	590 ACGCACCAGGAC	CGCACCAGGAC	ACACACCAGGAC ACACACCAGGAC
480 TCAAGTTC TCAAGTTC	** ****	580 CACCGTC	CACCGTCZ	CACCGTC
470 PAGACCCCGATG SAAGACCCCGATG	3AAGACCCCGAGG :******** *	570 GGTCAGCGTCCT	GGTCAGCGTCCT	GGTCAGCGTCCT
460 gagccage gagccage	:4******	560 Tratceter	TATCGTG	STACCGCGI STACCGCGI
450 GGTGGTAGACGT GGTGGTAGACGT	****** *****	550 TACAACAGCACA	TACAACAGCACA	TACAACAGCACG TACAACAGCACG
440 ACGTGCGT ACGTGCGT	** ****	540 AGACGCAG	AGACGCAG	AGACGCAG
430 BACCCCTGAGGTC BACCCCTGAGGTC	3ACCCCTGAGGTC **********	530 ACGAAGCCACGGG	CGAAGCCACGG	CATGCCCAGACGAAGGAAGGGAGAGGCAGGTACAACAGCACGTACGGGTGGTCAGCGTCCTCACCGTCACACACA
420 ITCTCCCGC ITCTCCCGC	######################################	520 TGCCCAG	TGCCCAG	TGCCCAGA
410 420 430 440 450 460 470 480 490 500 AGGACACCTCATGATGATCGTGAGGTCACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGAAATGGCYDO3_18 AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGTAGACGTGAGCCAGGAAGACCCCGATGTCAAGTTCAACTGGTAAATGGCYTO3_16 AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGATGGTGGTGGTGGTAGGTGGTGAGGTGGTGAGGTGGT	AGGACACCCTCATGATCTCCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACCTGAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGAAACGGcyno1_4 ************************************	510 520 530 540 550 560 570 580 590 600 cocede and considerate and companies and compa	CGCGGAGGTGCATCATGCCCAGAAGCCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAGGACTGGCTGcyno3_16	CGCGGAGGTGCATCATGCCCAGACGAAGCCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCGTCACACACA
_cyno3_18 _cyno3_16 _cyno1_3	_cyno1_4 ·	_cyno3_18	_cyno3_16	_cynol_3 _cynol_4

_cyno3_18 _cyno3_16

690

670

AACGGCAAGGAGTACACGTGCAAAGGTCTCCAAAAAGCCCTCCCGGCCCCCATCCAGAAACCATCTCCAAAAGGGCAAGCCAGGAGGGCAGGCCTCAGG

_cyno3_18 _cyno3_16

_cyno1_3 _cyno1_4

640

AACGGGAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAAACCATCTCCAAAAGACAACAGGGCAGCCCGAGAGCCTCAAG AACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAAACCATCTCCAAAAGACAAAGGCAGCCCCGAGAGCCTCAGG _cyno1_47

_cyno1_3

	_cyno3_18	_cyno3_16	_cyno1_3	_cyno1_4	
800	STGGAGTG	STGGAGTG	STGGAGTG	STGGAGTG	*****
190	GACATCGTC	GACATCGTC	GACATCGTC	GACATCGTC	******
780	TACCCCAGC	TACCCCAGC	TACCCCAGC	TACCCCAGC	******
770	PCAAAGGCTTC	CCCGTCCCGGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG	PCAAAGGCTTC	гсалавесттс	******
160	ACCTGCCTGG	ACCTGCCTGG	ACCTGCCTGG	ACCTGCCTGG	*******
750	SGTCAGCCTG	GTCAGCCTG	GTCAGCCTG	ветс авеств	*****
740	CAAGAACCAC	CAAGAACCAC	CAAGAACCAC	CAAGAACCAG	*****
730	AGGAGCTGAC	AGGAGCTGAC	AGGAGCTGAC	AGGAGCTGAC	******
720	ccercceec	ccercccee	SCGTCCCGG	CCGTCCCGGG	******
710	TETRCACCCTGCCCCCGGCGGGGGGGGGGGGGGAGCTGACCAGGTCAGCCTGACCTGCCTG	TGTACACCCTGCCC	TGTACACCCTGCCCCCGTCCCGGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG	TGTACACCCTGCCCCGGTCCCGGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG	新兴安斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯斯

_cyno3_18 _cyno3_16

_cyno1_3 _cyno1_4

FIG. 16G

		810	820	830	840	850	860	870	880	890	900	
_cyno3_18		GEAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCG	3CAGCCGGAG	ACACCTACAA	GACCACCCG	ccerecrea	ACTCCGACGG	CTCCTACTTC	CTCTACAGCA	AGCTCACCGTG	GACAAG	_cyno3_1£
_cyno3_16		GGAGAGCAGCGGGGAGCCGGAGAACACCTACAAGACCACCCCGCCCG	3CAGCCGGAG2	ACACCTACAA	GACCACCCGG	CCGTGCTGG	ACTCCGACGG	CTCCTACTTC	CTCTACAGCA	AGCTCACCGTG	GACAAG	_cyno3_16
_cyno1_3	,	GGAGAGCAGCGGGCAGCCGGAGAACACCTACAAAGACCACCCGTGCTGGACTCCGACGGCTCCTACTTCCTCTACAGCAAGCTCACGTGGACAAGcyno1_3	3CAGCCGGAG7	ACACCTACAA	GACCACCCCG	ccerecree.	ACTCCGACGG	CTCCTACTTC	CTCTACAGCA	AGCTCACCGTC	GACAAG	_cyno1_3
_cyno1_4		GGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCGCCCG	GCAGCCGGAG? *********	ACACCTACAA	GACCACCCCG	*************	ACTCCGACGG ********	CTCCTACTTC *******	: * * * * * * * * * * * * * * * * * * *	3CCGGAGAACACCTACAAGACCACCCGCCCGTGGACTCCGACGGCTCCTACTTCCTCTACAAGAAGGTCACGTGGAAG ********************************	3GACAAG	_cyno1_4
		910	920	930	940	950	960	970	980	066		
_cyno3_18	:	AGCAGGTGGCAGGGGAACGTCTTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAACACACTACCAGAAGAGGCCTCTCCCTGTCTCCCGGGTAAAcyro3_18	CAGGGGAACG	CTTCTCATGC	тссетоалес	ATTCAGGCTCT	SCACAACCAC	TACACCCAGA	AGAGCCTCTC	ccrercrece	GTAAA	_cyno3_18
_cyno3_16		AGCAGGTGGCAGCAGGGGAACGTCTTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCAGAAGAGCCTCTCCCTGTCTCCCGGGTAAACyno3_16	CAGGGGAACGS	CTTCTCATGC	тссетватес	ATGAGGCTCT	SCACAACCAC	TACACCCAGA	AGAGCCTCTC	CCTGTCTCCGG	GTAAA	_cyno3_16
_cyno1_3	:	AGCAGGTGGCAGCAGCAGCGGAACGTCTTCTCATGCTCCGTGATGCTCTGCACCACAACCACAACCAGAAGAGCCTCTCCCTGTCTCCCGGGTAAAcyno1_3	CAGGGGAACGI	CTTCTCATGC	rccercareca	ATGAGGCTCT	GCACAACCAC	тасасссава	AAGAGCCTCTC	ccrercreced	GTAAA	cyno1.3
_cyno1_4		AGCAGGIGGCAGCAGCAGCAACGICTICTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAcyno1_4	CAGGGGAACGI	CTTCTCATGC	TCCGTGATGC	ATGAGGCTCT	GCACAACCAC	TACACCCAGA	AGAGCCTCTC	CCTGTCTCCGG	GTAAA	_cyno1_4

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AA sequence angumem	iignimeni										
	10	20	30	40	20	09	70	80	90	100	
_cyno2_4	ASTROPSVFPLASSSRSTSESTAALGCLVKDYFPEPVTVSMNSCALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSSLGTQTYVCNVVHEPSNTKVDKRVEFCYNO2_4	SSRSTSESTAA	LGCLVKDYFF	EPVTVSWNSGA	LTSGVHTFP	AVLOSSGLYS	LSSVVTVPSS	SLGTQTYVCIVV	VHEPSINTKV	DKRVEF	_cyno2_4
cyno2_4cys	ASTROPSVFPLASCSRSTSESTAALGCLVKDVFPEPVTVSANSGALJSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTVVCNVVHEPSNTKVDKRVEF	CSRSTSESTAA	LGCLVKDYFP	EPVTVSWNSGA	LTSGVHTFP	AVLQSSGLYSI	LSSWVTVPSS	SLGTQTYVCNV	VHEPSNTKV	DKRVEF	_cyno2_4cys
cynods1	ASTROPSYFPLASCSRSTSQSTAALGCLVXDYFPEPYTVSWNSGALTSGVHTFQAVLQSSGLXSLSSVYTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFCYNO2_4ds	CSRSTSQSTAA	LGCLVKDYFF	EPVTVSWNSGA	LTSGVHTFQ	AVLOSSGLYS	LSSVVTVPSS	SLGTQTYVCNV	VHEPSIVIKV	DKRVEF	_cyno2_4ds
супо33	ASTROPSVFPLASCSRSTISQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLSSVVTVPSSSSLGTQTYVCNVVHEPSNTKVDKTVGL	CSRSTSQSTAA	LGCLVKDYFP	EPVTVSWNSGA	LTSGVHTFQ	AVLQSSGLYSI	LSSVVTVPSS	SLGTQTYVCNV	VHEPSNTKV	DKTVGL	_cyno33
_cyno35	ASTROPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFQAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGL	CSRSTSQSTAA	LGCLVKDYFF	EPVTVSWNSGA	LISGVHITE	AVLOSSGLYS	LSSVVTVPSS	SLGTQTYVCIV	VHEPSNTKV	DKTVGL	_cyno35
_cyno36	ASTROPSVFPLASCSRSTISQSTAALGCLVKDYFPEPVITVSMNSGALTISGVHTFQAVLQSSGLYSLSSVVTVPSSSSLGTQTYVCNVVHEPSNTKVDKRVGL	CSRSTSQSTAA	LGCLVKDYFF	EPVTVSWNSGA	LISGVHTFQ	AVLQSSGLYS	L.SSVVTVPSS.	SLGTQTYVCM	VHEPSIVITKV	DKRVGL	_cyno36
_cyno477	-STROPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVITVSMNSGALTSGVHITFPAVLQSSGLYSLSSVVITVPSSSLGTQTXVCNVVHEPSNIKVDKTVGL	CSRSTSQSTAA	LGCLVKDYFF	EPVTVSWNSGA	LISGVHIFF	AVLOSSGLYS	LSSVVTVPSS	SLGTOTYVCM	VHEPSIVIKY	DKTVGL	_cyno477
_cyno32	ASTROPSUPPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALI'SGVHTFQAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGL	CSRSTSQSTAA	LGCLVKDYFF	EPVTVSWNSGA	LISGVHIFQ	AVLQSSGLYS.	LSSVVTVPSS	SLGTQTYVCM	VHEPSINTKV	DKRVGL	_cyno32
cyno686	-STKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSmNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTVVCNVVHEPSNTKVDKRVEFCYDO686	CSRSTSESTAA	LGCLVKDYFF	EPVTVSWNSGA	LTSGVHTFP	AVLOSSGLYS	LSSVVTVPSS	SLGTQTYVCN	VHEPSIVTK	DKRVEF	_cyno686
_cyno439	ASTROPSVFPLVSCSRSTSBSTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTVVCNVVHEPSNTKVDKRVEF	CSRSTSESTAA	LGCLVKDYFF	EPVTVSWNSGA	LTSGVHTFP	AVLQSSGLYS	LSSVVTVPSS	SLGTQTYVCNV	VHEPSINTKV	DKRVEF	_cyno439
_cyno1_4	ASTIKOPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSMNSGALTISGVHTFPAVLQSSGLYSLSSVVTVPSSSSLGTQTVVCNVNHKPSNTKVDKRVEL	SSRSTSESTAA	LGCLVKDYFF	EPVTVSWNSGA	LTSGVHTFP	AVLQSSGLYS.	LSSVVIIVPSS	SLGTQTYVCIN	NHKPSNTKV	DKRVEI	_cynol_4
_cyno1_3	ASTIKGPSUFPLAPSSRSTSESTAALGCLUKDYFPEPVTVSMNSGALITSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTVVCNVNHKPSNTKVDKRVEL	SSRSTSESTAA	LGCLVKDYFF	EPVTVSWINSGA	LISGVHTFP	AVLQSSGLYS	LSSWVTVPSS	SLGTQTYVCNV	NHKPSNTKV	DKRVEI	_cyno1_3
_cyno3_18	ASTROPSVFPLAPSSRSTSESTAALGCIVIOYFPEPVTVSMNSGSLTSGVHTFPAVLQSSGLYSLSSVVTVPSSSSLGTQTYVCNVNHKPSNTKVDKRVEL	SSRSTSESTAA	LGCLVKDYFF	EPVTVSWNSGS	LTSGVHTFP	AVLOSSGLYS	L.SSVVITVPSS.	SLGTQTYVCW	NHKPSNTK	DKRVEI	_cyno3_18
_cyno3_16	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSANISGSLTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEICYNO3_16	SSRSTSESTAA	LGCLVKDYFF	EPVTVSWNSGS	LISGVHTFP	AVLOSSGLYS	L.SSVVTVPSS.	SLGTQTYVCM	NHKPSNTKV	DKRVEI	_cyno3_16
	在 经存款证据 计多数分类 化二甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基甲基	****	****	*****	*****	*******	****	********	*****	. * **	

	110	-	120	130	140	150	160	170	180	190 .	200	
cyno2_4	TPPC	PPCPAP	ELLGGPSV	FLEPPKPKI	JULKI SRTPE	VICVVVDVSQ	EDPEVOFNWY	TPPCPPCPAPELLGGPSVFLFPPKPXDYLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVIJTHQDWL	KPREROFINS	PYRVVSVLTV	THODWL	_cyno2_4
cyno2 4cys	TPPCI	PPCPAP	ELLGGPSV	FLEPPKPKI	TLMISRTPE	TVTCVVVDVSQ	EDPEVQFNWY	TPPCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWL	KPRERQFNS	PYRVVSVLTV	THODWL	_cyno2_4cys
cynods1	TPPCI	PPCPAP	ELLGGPSV	FLFPPKPKI	OFLMISRTPE	VTCVVVDVSQ	EDPEVQFNWY	TPPCPAPELLIGGPSVFLFPPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWL	KPREROFINS	PYRWSVLTV	THODWL	cyno2_4ds
cyno33	PCRS!	PCPPCPA-	ELLGGPSV	FLEPPKPKI	OTLMI SRIPE	TVTCVVVDVSQ	EEPDVKFNWY	PCRSTCPPCPA-ELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKENWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLCYNO33	KPREEQFNS	FYRVVSVLTV	THODWL	_cyno33
_cyno35	PCRS!	rCPPCPA-	ELLGGPSV	FLFPPKPKI	OTLMI SRIPE	TVTCVVVDVSQ	EEPDVKFNWY	PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDÖVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL	KPREEQĖNS	PYRWSVLTV	THODWL	_cyno35
	PCRS:	ICPPCPA-	ELLGGPSV	PLEPPKPK	OTLMISRTPE	TVTCVVVDVSQ	EEPDVKFNWY	PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMLSRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL	KPREEQFINS	PYRVVSVLTV	THODWL	_cyno36
_cyno477	PCRS	TCPPCPA-	ELLGGPSV	FLFPPKPK	DYLMISRTPE	VTCVVVDVSQ	EEPDVKFNWY	PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMLSRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL	KPREEQFINS	PYRVVSVLTV	THODWL	_cyno477
_cyno32	PCRS!	TCPPCPA-	ELLGGPSV	FLFPPKPK	OTLAI SRIPE	TVTCVVVDVSQ	EEPDVKFNWY	PCRSTCPPCPA-ELLGGPSVFLFPPKPKDJIMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLIVTHQDML	KPREEQFNS	IYRWSVLTV	THODWL	_cyno32
	-TRPCDDTTP	PCPPCPAP	ELLGGPSV	FVPPPKPK	PYLMISRTPE	vicvvvďsc	EDPEVOFNWY	-TRPCDDTTPPCPPCPAPELLGGPSVFVFPPREVDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGAEVHHAQTKPRETQYNSTYRVVSVLITVTHQDWL	KPRETOYNS	FYRWSVLTV	THODWL	_cyno686
cyno439	-TRPCDDTTP1	PCPPCPAP	ELLGGPSV	FVFPPKPK	OTLMI SRTPE	TVTCVVVDVSQ	EDPEVQFNWY	-TRECDOTTEPCEPCEAPELLGGESUFVFFPEKEKDILMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAQTKPRERQFNSTYRVVSVLIVIHQDWL	TKPRERQFNS	PYRVVSVLTV	THODWL	_cyno439
cynol 4	KTCGGGSKPP!	ICPPCPAP	ELLGGPSV	FLFPPKPK	DTLMISRTPE	TVTCVVVDVSQ	EDPEVQFINY	KTCGGGSKPPTCPPCPAPELLIGGPSVFLFPPKPKDYLMLSRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL	KPRETOYNS	TYRVVSVLTV	THODWL	_cyno1_4
_cyno1_3	KTCGGGSKPP	TCPPCPAP	ELLGGPSV	FLFPPKPK	DTLMISRTPE	SVTCVVVDVSQ	EDPEVQFNWY	KTCGGGSKPPTCPPCPAPELLGGPSVFLFPPKPKDTLMLSRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL	TKPRETQYNS	LYRVVSVLTV	THODWL	_cyno1_3
_cyno3_18	TCGGGSKPP	TCPPCPAP	ELLGGPSV	FLFPPKPK	DTLMISRTPE	SVICVVVDVSC	EDPDVKFNWY	-TCGGGSKRPTCPPCPAPELLGGPSVFLFPPKPKDYLMLSRTPEVTCVVVDVSQEDPDVKRNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL	KPRETQYNS	TYRVVSVLTV	THODWL	_cyno3_18
_cyno3_16	KTCGGGSKPP	TCPPCPAP	ELLGGPSV	FLFPPKPK	DTLMISRTPE	SVTCVVVDVSC	EDPDVKENWY	KTCGGGSKPPTCPPCPAPELLGGPSVFLFPRKPKDTLMLSRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL	TKPRETQYNS	TYRWSVLTV	THODWL	_cyno3_16
		*	******	*****	*******	**********	****	经分额条件的非正常的现在分词 计记录记录记录 "我不是我的话,我不是一种,我们也是不是一种,我们是我们的是我们的是我的的,我们是我们的人,我们是我们的人,我们们们的人,我们们们的人,我们们们的人,我们	**** ****	*******	*****	

	210	220	230	240	250	260	270	280	290	300	
_cyno2_4	NGKEYTCKVSNKGLPAPIEKTISKAKG QPREPQVYILPPPQEELIKNQVSLICLVTGFYPSDIAVEWESNGQPENTYKITPPVLDSDGSYFLYSKLIVDKcyno2_4	PAPIEKTISE	CAKGOPREPO	TILPPPQEEL	TRNOVSLTCI	VTGFYPSDIA	VEWESNGOPE	VITYKITIPPVI.	DSDGSYFLYSKL	TVDK	cyno2_4
_cyno2_4cys	ngkeytckvsnkglpapiektiskakg oprepovyilpppqeeltknqvsltclvtgfypsdiavemesngopentykttppvldsdgsyflysklivdk _cyno2_4cys	PAPIEKTISE	CAKG QPREPQ I	YILPPPQEEL	TRNQVSLTCI	VTGFYPSDIA	VEWESNGQPE	VI'YKT'TPPVI.	DSDGSYFLYSKL	TVDK.	_cyno2_4cys
_cynods1	NGKEYTCKVSNKGLPAPIEKTISKAKGOPREPOVYILPPPOEELTKNOVSLICLVIGFYPSDIAVEWESNGOPENTYKTTPPVLDSDGSYFLYSKLIVDK	PAPIEKTISE	CAKGOPREPO	VILPPPQEEL	TRNOVSLICE	VIGEYPSDIA	VEWESNGOPE	VIYKT TPPVL	DSDGSYFLYSKL		_cyno2_4ds
_cyno33	NGKEYTCKVSNKALPAPKQKTVSKTKG QPREPQVYTLPPPREELIKNQVSLICLVKGFYPSDIVVEWASNGQPENTYKTTPPVLDSDGSYFLYSKLIVDK	PAPKQKTVSI	TKG OPREPOT	YYLPPPREEL	TKWQVSLTCI	VKGFYPSDIV	Venasngope	VITYKITIPPVI.	DSDGSYFLYSKL		_cyno33
_cyno35	NGKEYTCKVSNKALPAPKOKTVSKTKGQPREPQVYTLPPPREELIKNQVSLICLVKGFYPSDIVVENASNGQPENTYKTTPPVLDSDGSYFLYSKLIVDKCyno35	PAPKOKTVSI	CTKG QPREPQI	YTLPPPREEL	TRNOVSLICE	VKGFYPSDIV	VEWASNGOPE	VITYKITIPPVL	DSDGSYFLYSKL	TVDK	cyno35
_cyno36	NGKEYTCKVSNKALPAPKQKTVSKTKG QPREPQVYTLPPPREELIKNQVSLIYCLVKGFYPSDIVVENASNGQPENTYK TT PPVLDSDGSYFLYSKLIYDK	PAPKOKTVSI	(TKGQPREPQ)	NTLPPPREEL	TKNOVSLÍCI	VKGFYPSDIV	VEWASNGOPE	VITYKTITPPVI.	DSDGSYFLYSKL		_cyno36
_cyno477	NGKEYTCKVSNKALPAPROKTVSKTKGOPREPQVYTLPPPREELIKNQVSLITCLIKGFYPSDIVVEMASNGOPENTYKTTPPVLDSDGSYFLYSKLIVDK	PAPROKTVS	CTKG OPREPO	TTLPPPREEL	TRADVSLICI	IKGFYPSDIV	VEWASNGOPE	WYYKTTPPVI.	DSDGSYFLYSKL	TVDK	_cyno477
_cyno32	NGKEYTCKVSNKGLPAPIEKTISKAKG <i>QPREPQVYILPPPQEELIK</i> NQ <i>VSLICLVTGFYPSDLAVENESNGQPENTYRTTPPVLDSDGSYFLYSKLIVDK</i>	PAPIEKTIS	CAKGOPREPOT	YILPPPQEEL	TRNOVSLICE	VTGFYPSDLA	VEWESNGOPE	WTYKTTPPVL.	DSDGSYFLYSKL		_cyno32
_cyno686	NGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK	PAPIOKTIS	DKGOPREPO	TTLPPSREEL	TKNOVSLTCI	VKGFYPSDIV	VEWESSGOPE	WYXKTTPPVL	DSDGSYFLYSKL		_cyno686
_cyno439	NGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELIFNQVSLITCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLIVDK	PAPIQKTISE	DKGQPREPQ 1	PYTLPPSREEL	TKNOVSLTCL	VKGFYPSDIV	Vewessgope	VITYKITIPPVI.	DSDGSYFLYSKL		_cyno439
_cyno1_4	NGKEYTCKVSNKALPAPIQKTI SKDKGQPREPQVYTLPPSREELTKNQVSLITCLVRGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLITVDK	PAPIQKTIS	DKGQPREPQ	YTLPPSREEL	TKNOVSLTCI	VKGFYPSDIV	VEWESSGOPE	VIYKTTPPVL	DSDGSXFLYSKL		_cyno1_4
_cyno1_3	NGKEYTCKVSNKALPAPIQKTISKDKG Q prep qvytlppsreelitnqqvsliclvrgfypsdiv vewess gqpentyktttppvldsdgsyflyskli tvdk	PAPIQKTISE	DKGQPREPQ 1	YTLPPSREEL	TKNQVSLTCL	VKGFYPSDIV	Vewessgope	VIYKITIPPVL	DSDGSYFLYSKL		_cyno1_3
_cyno3_18	NGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLICLVRGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDR	PAPIOKTISE	COKG OPREPO	YTLPPSREEL	TKWOVSLICE	VKGFYPSDIV	VEWESSGOPE	VIYKITPPVL	DSDGSYFLYSKL		_cyno3_18
_cyno3_16	NGKEYTCKVSNKALPAPIQKTISKDKG QPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK	PAPIQKTISE	DKGQPREPQ 1	YTLPPSREEL	TKNOVSLTCL	VKGFYPSDIV	Vewessgope	VIYKTTPPVL.	DSDGSYFLYSKL		_cyno3_16
	**** ********		*****	***	*******	******	**** * ***	******	"我我,我我们是我的的人,我们我们的人们的人们的人们的人们,我们也不是我们,我们的人们的人们的现在分词的人的现在分词的人们的人们的人们的人们的人们的人们的人们们们们们们们们们们们们们们们们们们	* *	

3 6 6 6	SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK	SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK _cyno2_4 SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK _cyno2_4cys
ଅଧି	SKWQQGNTFSCSVMHEALHNHTTQKSLSVSFGKCYDOZ_4GS SRWQQGNTFSCSVMHEALHNHTTQKSLSVSFGKCYDO33	K _cyno2_4ds K _cyno33
	SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGKCYDO35 SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGKCYDO36	K _cyno35 K _cyno36
6 3 63	SRWQQGNTFSCSVMHEALHNHYTQKSLSFGK _Cyno477 SRWQQGNTFSCSVMHEALHNHYTQKSLSVSFGK _Cyno32	ξ _cyno477ζ _cyno32
Ø. Ø	SRWQQGNVFSCSVMEEALENHYTQKSLSLSPGKCyno686 SRWQQGNVFSCSVMEEALENHYTQKSLSLSPGKCyno439	σγπο686σγπο439
5 1 53	SRWQQGNVFSCSTVMEEALENHYTQKSLSLSPGKCyno1_4 SRWQQGNVFSCSTVMEEALENHYTQKSLSLSPGKCyno1_3	x _cyno1_4 x _cyno1_3
63 63	SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK _cyno3_18 SRWOOGNVFSCSVMHEALHNHYYTQKSLSLSPGK cyno3_16	cyno3_18 cyno3_16

FIG 17F

26/30

A. H	eavy	Chain Variat	ole Region N	ucleotide Se				
H1	1	CACCMMCACC	macmaa ama	mcccccx ccc	FR1	CTGGGGGGTC	CCTCACACTC	60
H2	1					CTGGGGGGTC		60
H3	1					CTGGGGGGTC		60
H4	1					CTGGGGGGTC		60
H5	1					CTGGGGGGTC		60
н6	1					CTGGGGGGTC		60
H7	1					CTGGGGGGTC		60
нв	1					CTGGGGGGTC		60
н9	ī					CTGGGGGGTC		60
H10	1	GAGGTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H11	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H12	1					CTGGGGGGTC		60
H13	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H14	1					CTGGGGGGTC		60
					CDR1			
H1	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTC TGGGT	TCGCCAGGCT	120
H2	61					TGTTC TGGGT		120
н3	61					TGTTCTGGGT		120
H4	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTC TGGGT	TCGCCAGGCT	120
H5	61						TCGCCAGGCT	120
н6	61						TCGCCAGGCT	120
H7	61						TCGCCAGGCT	120
H8	61						TCGCCAGGCT	120
H9	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTC TGGGT	TCGCCAGGCT	120
H10	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120
H11	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120
H12	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120
H13	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120
H14	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120
		ਾਜ ਪਤ	R2			CDR2		
H1	121			GGTATCA GGT	ATTGGTACTG		AAACTATGCA	180
H2	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180
нз							AAGCTATGCA	180
H4							AAACTATGCA	180
н5							AAACTATGCA	180
н6							AAACTATGCA	180
H7	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA GGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180
Н8	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA GGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180
н9	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180
H10	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA GGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180
H11	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA GGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180
H12							AAGCTATGCA	180
H13							AAGCTATGCA	180
H14	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180

27/30

-						FR3		
	101	GACTCCGTGA	**************************************	C አ C C አ ጥርጥር C	ACACACAATG		CTTGTATCTT	240
H1	TRT	GACTCCGTGA	AGGGCCGAT1	CACCATCICC	ACACACAATC	CCAAGAACTC	CTTGTATCTT	240
H2	TRT	GACTCCGTGA	AGGGCCGATT	CACCATCICC	ACACACAATC	CCAAGAACTC	CTTGTATCTT	240
н3	181	GACTCCGTGA	AGGGCCGATI	CACCATCICC	ACAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H4	TRT	GACTCCGTGA	MGGGCCGA11	CACCATCICC	ACACACAATG	CCAAGAACTC	CTTGTATCTT	240
H5	181	GACTCCGTGA	ACCCCCATT	CACCATCICC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H6	181	GACTCCGTGA	ACCCCCATI	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H7	181	GACTCCGTGA	AGGGCCGATT	CACCATCICC	ACACACAATG	CCAAGAACTC	CTTGTATCTT	240
H8	181	GACTCCGTGA	AGGGCCCATI	CACCATCICC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H9	T8T	GACTCCGTGA	*CCCCCVUT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H10	TRI	GACTCCGTGA	ACCCCCATT	CACCATCICC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H11	T8T	GACTCCGTGA	ACCCCCATT	CACCATCICC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H12	,101 TRT	GACTCCGTGA	AGGGCCGAII	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H13	TRT	GACTCCGTGA	AGGGCCGATI	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H14	TRT	GACTCCGTGA	AGGGCCGAII	CACCATCTCC	110110110111110			
	0.41	CAAATGAACA	CCCCCCACACC	CCACGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H1	241	CAAATGAACA	CCCTGAGAGC	CCACCACATG	CCTCTCTATT	ACTGTGCAAG	AGGGAGGTAC	300
H2	241	CAAATGAACA	CCCTGAGIGC	CCACCACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H3	241	CAAATGAACA	CCCTGAGAGC	CCACCACATG	CCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H4	241	CAAATGAACA	CCCTGAGAGC	CCACCACATC	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H5	241	CAAATGAACA	CCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H6	241	CAAATGAACA	CCCTGAGAGC	CCACCACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H7	241	CAAATGAACA	CCCTGAGAGC	CGACCACATG	CCTCTCTATT	ACTGTGCAAG	AGGGAGGTAC	300
H8	241	CAAATGAACA	CCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H9	241	CAAATGAACA	CCCTGAGAGC	CCACCACATA	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H10	241	CAAATGAACA	CCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H11	241 741	CAAATGAACA	CCCTCAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H12 H13	241	CAAATGAACA	CCCTGAGTGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
H14	241	CAAATGAACA	CCCTCAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC	300
HT4	247	CAAAIGAACA	000101100	00.00				
		CDR3			FR4			
н1	3.01	TACTTTGACT	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 345	S (SEQ ID N	NO:47)
H2	301	TACTTCACCC	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 345	SEQ ID N	10:48)
H3	301	TGGTACAACA	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 345	S (SEQ ID N	NO:49)
H4	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 345	SEQ ID 1	٥0:50)
H5	301	TACTTCACGA	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCI	CCTCA 345	S (SEQ ID 1	NO:51)
н6	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 34	5 (SEQ ID 1	NO:52)
H7	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 34		
H8	301	TGGTTCCCGT	GG TGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 34	5 (SEQ ID 1	10:54)
но Н9	3 N 1	TGGTTCCCGT	GGTGGGGGCCA	GGGAACCCTC	GTCACCGTCT	CCTCA 34	5 (SEQ ID I	NO:55)
H10	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA 34	5 (SEQ ID I	NO:56)
H11	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTC	GTCACCGTCT	CCTCA 34	5 (SEQ ID 1	NO:57)
H12	3 N 1	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTC	GTCACCGTCT	CCTCA 34	5 (SEQ ID 1	NO:58)
H13	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTC	GTCACCGTCT	CCTCA 34		
H14	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCT	GTCACCGTC	CCTCA 34	5 (SEQ ID	NO:60)
UT#	501			-				

FIG. 18B

B. Heavy Chain Variable Region Amino Acid Sequences

FR4 QGTLVTVS			
CARGRYYFDYWGQGTLVTVS	PW	MāxM	Ma
FR2 CDR3 FR4 VRQAPGKGLEWVSGIGTGGATNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMAVYYCARGRXYKDYWGQGTLVTVS			Ma
CDR2 WVSGIGTGGATNYADSVKGRFT			
FR2 RQAPGKGLEV			
CDR1 FSRNAMEWV	- 1 1 i		
FR1 EVQLVQSGGGLVHPGGSLRLSCAGSGFTFSRNAMEW			EÀAA
H 12 H	H4 H5 H6	H7 H8 H9 H10	H11 412 13

9:0	ID NO:62)	30:6	VO:64	10:65	30:6	10:67	VO: 68	30:6	70:7	NO:7	NO:	NO: 7	ID NO:74	
(SEQ I	(SEQ I	(SEQ I	(SEQ I	(SEQ	(SEQ	(SEQ I	(SEQ I	(SEQ I	(SEQ	= (SEQ	(SE	= (SEQ	= (SEQ	
HI =	H2 =	H3 =	H4 =	H5 =	= 9H	H7 =	H8 =	H9 =						

PCT/US2004/037241

29/30

A. Light Chain Variable Region Nucleotide Sequences

L1	1	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L2	1	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L3	1	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCGGGGGA	AAGAGCCACC	60
L4	1	GAAATTGTGA	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L5	1	GATATTGTGC	TGACCCAGTC	TCCAGCCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L6	1	GATATTGTGC	TGACGCAGAC	TCCAGCCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
				CDR1				
L1	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AGCAGCTACT	TAGCCTGGTA	CCAGCAGAAA	120
L2	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AACAGCTACT	TAGCCTGGTA	CCAGCAGAAA	120
L3	61	CTCTCCTGCA	GGGCCAGTCA	GACTGTTAAC	AGCGACTACT	TAGCCTGGTA	CCAGCAGAAA	120
L4	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AGCGACTACT	TAGCCTGGTA	CCAGCAGAAA	120
L5	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAAC	AGCAACTACT	TAGCCTGGTA	CCAGCAGAAA	120
L6	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTGGC	AGCAGCTACT	TAGCCTGGTA	CCAGCAGAGA	120
						_		
			FR2		CDR			100
L1	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTTT	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	180
L2	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCCA	GCAGGGCCCC	TGGCATCCCA	180
L3	121	CCGGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	180
L4	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCTA	GCAGGGCCTC	TGGCATCCCA	180
L5	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTACATCCT	ACAGGGCCAC	TGGCATCCCA	180
L6	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCG	180
					ED3			
	101	an an aamman	amacan amaa	CMCMCCCA CA	FR3	TCACCATCAG	ראכאריזיככאכ	240
L1 L2	101	CACACCCOOCA	GIGGCAGIGG	CUCUCCCACA	CACTICACIC	TCACCATCAG	CAGACTGGAG	240
L2	TOT	CACACCTTCA	CTCCCACTCC	CTCTGGGACA	CACTICACIC	TCACCATCAG	CAGACTGGAG	240
L3	101	CACAGGITCA	CITCGCAGTGG	CTTTGGGACA	CACTTCACTC	TCACCATCAG	CAGACTGGAG	240
L5	101	CACAGGIICA	CTCCCACTCC	CTCTCCCACA	CACTTCACTC	TCACCATCAC	CAGACTGGAG	240
L6	101	CACACCTTCA	GTGGCAGTGG	CTCTGGGACA	GACTTCACTC	TCACGATCAG	CAGACTGGAG	240
110	101	GACAGGIICA	GIGGCRGIGG	310100011011	0.101101010	101104111 5111		
						CDR3		
L1	241	CCTGAAGATT	TTGCAGTGTA	TTACTGTCAG	CAGTATGGTA	GCTCACCTCC	GTGGACGTTC	300
L2	241	CCTGAAGATT	TTGCAGTGTA	TTACTGTCAG	CAGTATGATC	ACTCAGCAGG	GTGGACGTTC	300
L3	241	CCTGAAGATT	TTGCAGTCTA	TTACTGTCAG	CAGTATGGTA	GGTCACCTCC	GTGGACG TTC	300
L4	241	CCTGAAGATT	TTGCAATATA	TTACTGTCAG	CAGTATGGTA	GCTCACCTCC	GTGGACG TTC	300
L5	241	CCTGAAGATT	TTGCAGTGTA	TTACTGTCAG	CAGTATGGTA	GCTCACCACC	GTGGACG TTC	300
L6	241	CCTGAAGATT	TTGCAGTGTA	TTATTGTCAG	CAGTATGGAA	GTTCACCTCC	GTGGATG TTC	300
			FR4					
L1		GGCCAAGGGA						
L2		GGCCAAGGGA			27 (SEQ ID			
L3		GGCCAAGGGA			27 (SEQ ID			
L4		GGCCAAGGGA			27 (SEQ ID	· ·		
L5		GGCCAAGGGA			27 (SEQ ID	•		
L6	301	GGCCAAGGGA	CCAAGGTGGA	GATCAAA 3	27 (SEQ ID	NO:80)		

FIG. 19A

B. Light Chain Variable Region Amino Acid Sequences

CDR3 FR4	CGSSPFWIF GOGLAVELA			KL		i
FR3	EIVITOSPGTLSLSPGERATLSCRASOSVSSSTLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCQXGSSFFWTFGGGLAVELA			XXXXXX		DT-A
CDR2	LIFGASSRATG	~d~~~~~~X~~~]		- * * - * - * - * - * - * - * - * - * -	
FR2	AWYQQKPGQAPRLI				1111111111111	R
CDR1	SCRASQSVSSSYI	N			N-N	·
FRI	EIVLTQSPGTLSLSPGERATL			-QW	DA	DT-A
	<u> 11</u>	172	E3	17	15	176

L1 = (SEQ ID NO:81) L2 = (SEQ ID NO:82) L3 = (SEQ ID NO:83) L4 = (SEQ ID NO:84) L5 = (SEQ ID NO:85) L6 = (SEQ ID NO:85)